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1631

TECH CENTER 1600/2900

S. Szw  
RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/533,466

DATE: 03/29/2001  
TIME: 16:16:47

Input Set : A:\21416942.app  
Output Set: N:\CRF3\03292001\I533466.raw

ENTERED

3 <110> APPLICANT: COLLART, FRANK R.  
4 HUBERMAN, ELIEZER  
5 JOACIMIAK, ANDRZEJ  
6 ZHANG, RONGGUANG  
7 WESTBROOK, EDWIN M.  
9 <120> TITLE OF INVENTION: USE OF CRYSTAL STRUCTURE OF BACTERIAL IMP DEHYDROGENASE  
10 TO DESIGN INHIBITORS OF BACTERIAL GROWTH  
12 <130> FILE REFERENCE: 21416/90042  
14 <140> CURRENT APPLICATION NUMBER: 09/533,466  
15 <141> CURRENT FILING DATE: 2000-03-23  
17 <160> NUMBER OF SEQ ID NOS: 23  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
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23 <212> TYPE: PRT  
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34 <213> ORGANISM: Bacillus subtilis  
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43 <212> TYPE: PRT  
44 <213> ORGANISM: Escherichia coli  
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52 <211> LENGTH: 15  
53 <212> TYPE: PRT  
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63 <212> TYPE: PRT  
64 <213> ORGANISM: Mycobacterium tuberculosis  
66 <400> SEQUENCE: 5  
67 Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val  
68 1 5 10 15

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Input Set : A:\21416942.app  
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71 <210> SEQ ID NO: 6  
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81 <210> SEQ ID NO: 7  
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83 <212> TYPE: PRT  
84 <213> ORGANISM: Mus musculus  
86 <400> SEQUENCE: 7  
87 Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys Gly Arg  
88 1 5 10 15  
91 <210> SEQ ID NO: 8  
92 <211> LENGTH: 15  
93 <212> TYPE: PRT  
94 <213> ORGANISM: Arabidopsis thaliana  
96 <400> SEQUENCE: 8  
97 Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala Cys Gly Arg  
98 1 5 10 15  
101 <210> SEQ ID NO: 9  
102 <211> LENGTH: 15  
103 <212> TYPE: PRT  
104 <213> ORGANISM: Leishmania donovani  
106 <400> SEQUENCE: 9  
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108 1 5 10 15  
111 <210> SEQ ID NO: 10  
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113 <212> TYPE: PRT  
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122 <211> LENGTH: 15  
123 <212> TYPE: PRT  
124 <213> ORGANISM: Drosophila melanogaster  
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131 <210> SEQ ID NO: 12  
132 <211> LENGTH: 23  
133 <212> TYPE: PRT  
134 <213> ORGANISM: Streptococcus pyogenes  
136 <400> SEQUENCE: 12  
137 Met Ala Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala  
138 1 5 10 15

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Input Set : A:\21416942.app  
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140 Asp Lys Leu Val Pro Glu Gly  
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146 <212> TYPE: PRT  
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151 1 5 10 15  
153 Asp Lys Leu Val Pro Glu Gly  
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158 <211> LENGTH: 24  
159 <212> TYPE: PRT  
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164 1 5 10 15  
166 Ala Asn Lys Leu Val Pro Glu Gly  
167 20  
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171 <211> LENGTH: 21  
172 <212> TYPE: PRT  
173 <213> ORGANISM: Bacillus subtilis  
175 <400> SEQUENCE: 15  
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177 1 5 10 15  
179 Phe Val Pro Glu Gly  
180 20  
183 <210> SEQ ID NO: 16  
184 <211> LENGTH: 30  
185 <212> TYPE: PRT  
186 <213> ORGANISM: Mycobacterium tuberculosis  
188 <400> SEQUENCE: 16  
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192 Ala Asp Asp Ala Leu Ser Glu Asp Lys Leu Val Pro Glu Gly  
193 20 25 30  
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198 <212> TYPE: PRT  
199 <213> ORGANISM: Homo sapiens  
201 <400> SEQUENCE: 17  
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203 1 5 10 15  
205 Lys Ile Lys Val Ala Gln Gly  
206 20  
209 <210> SEQ ID NO: 18  
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Input Set : A:\21416942.app  
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211 <212> TYPE: PRT  
212 <213> ORGANISM: Mus musculus  
214 <400> SEQUENCE: 18  
215 Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala Asp  
216 1 5 10 15  
218 Lys Ile Lys Val Ala Gln Gly  
219 20  
222 <210> SEQ ID NO: 19  
223 <211> LENGTH: 27  
224 <212> TYPE: PRT  
225 <213> ORGANISM: Arabidopsis thaliana  
227 <400> SEQUENCE: 19  
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229 1 5 10 15  
231 Asn Glu Met Asp Lys Met Lys Val Ala Gln Gly  
232 20 25  
235 <210> SEQ ID NO: 20  
236 <211> LENGTH: 27  
237 <212> TYPE: PRT  
238 <213> ORGANISM: Leishmania donovani  
240 <400> SEQUENCE: 20  
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242 1 5 10 15  
244 Ser Glu Ser Asp Ser Val Leu Val Ala Gln Gly  
245 20 25  
248 <210> SEQ ID NO: 21  
249 <211> LENGTH: 21  
250 <212> TYPE: PRT  
251 <213> ORGANISM: Drosophila melanogaster  
253 <400> SEQUENCE: 21  
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255 1 5 10 15  
257 Lys Ile Ala Gln Gly  
258 20  
261 <210> SEQ ID NO: 22  
262 <211> LENGTH: 23  
263 <212> TYPE: PRT  
264 <213> ORGANISM: Saccharomyces cerevisiae  
266 <400> SEQUENCE: 22  
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268 1 5 10 15  
270 Ala Val Gln Val Ala Gln Gly  
271 20  
274 <210> SEQ ID NO: 23  
275 <211> LENGTH: 477  
276 <212> TYPE: PRT  
277 <213> ORGANISM: Artificial Sequence  
279 <220> FEATURE:  
280 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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Input Set : A:\21416942.app  
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281        polypeptide  
283 <220> FEATURE:  
284 <221> NAME/KEY: MOD\_RES  
285 <222> LOCATION: (1)...(477)  
286 <223> OTHER INFORMATION: "Xaa" represents selenomethionine  
288 <400> SEQUENCE: 23  
289 Ser Asn Trp Asp Thr Lys Phe Leu Lys Gly Tyr Thr Phe Asp Asp  
290     1               5               10               15  
292 Val Leu Leu Ile Pro Ala Glu Ser His Val Leu Pro Asn Glu Val Asp  
293     20              25              30  
295 Leu Lys Thr Lys Leu Ala Asp Asn Leu Thr Leu Asn Ile Pro Ile Ile  
296     35              40              45  
W--> 298 Thr Ala Ala Xaa Asp Thr Val Thr Gly Ser Lys Xaa Ala Ile Ala Ile  
299     50              55              60  
W--> 301 Ala Arg Ala Gly Gly Leu Gly Val Ile His Lys Asn Xaa Ser Ile Thr  
302     65              70              75              80  
304 Glu Gln Ala Glu Glu Val Arg Lys Val Lys Arg Ser Glu Asn Gly Val  
305     85              90              95  
307 Ile Ile Asp Pro Phe Phe Leu Thr Pro Glu His Lys Val Ser Glu Ala  
308     100             105             110  
W--> 310 Glu Glu Leu Xaa Gln Arg Tyr Arg Ile Ser Gly Val Pro Ile Val Glu  
311     115             120             125  
W--> 313 Thr Leu Ala Asn Arg Lys Leu Val Gly Ile Ile Thr Asn Arg Asp Xaa  
314     130             135             140  
W--> 316 Arg Phe Ile Ser Asp Tyr Asn Ala Pro Ile Ser Glu His Xaa Thr Ser  
317     145             150             155             160  
319 Glu His Leu Val Thr Ala Ala Val Gly Thr Asp Leu Glu Thr Ala Glu  
320     165             170             175  
322 Arg Ile Leu His Glu His Arg Ile Glu Lys Leu Pro Leu Val Asp Asn  
323     180             185             190  
325 Ser Gly Arg Leu Ser Gly Leu Ile Thr Ile Lys Asp Ile Glu Lys Val  
326     195             200             205  
328 Ile Glu Phe Pro His Ala Ala Lys Asp Glu Phe Gly Arg Leu Leu Val  
329     210             215             220  
331 Ala Ala Ala Val Gly Val Thr Ser Asp Thr Phe Glu Arg Ala Glu Ala  
332     225             230             235             240  
334 Leu Phe Glu Ala Gly Ala Asp Ala Ile Val Ile Asp Thr Ala His Gly  
335     245             250             255  
337 His Ser Ala Gly Val Leu Arg Lys Ile Ala Glu Ile Arg Ala His Phe  
338     260             265             270  
340 Pro Asn Arg Thr Leu Ile Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala  
341     275             280             285  
343 Arg Ala Leu Tyr Asp Ala Gly Val Asp Val Val Lys Val Gly Ile Gly  
344     290             295             300  
346 Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val Pro  
347     305             310             315             320  
349 Gln Val Thr Ala Ile Tyr Asp Ala Ala Val Ala Arg Glu Tyr Gly  
350     325             330             335  
352 Lys Thr Ile Ile Ala Asp Gly Gly Ile Lys Tyr Ser Gly Asp Ile Val

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/533,466

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TIME: 16:16:48

Input Set : A:\21416942.app  
Output Set: N:\CRF3\03292001\I533466.raw

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L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:361 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23